RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/049,967C*
Source: *PCT*
Date Processed by STIC: *6/2/05*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u>
<u>VERSION 4.2.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U S PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS
  http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office; and instead should be sent via the following to the indicated addresses

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O Box 1450, Alexandria, VA 22313-1450 ,
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U S Patent and Trademark Office. Mail Stop Sequence. Customer Window Randolph Building, 401 Dulany Street
   Alexandria, VA 22314

Revised 01/24/05

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/049,967

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics / Wrapped Aminos — The number next at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .): this will prevent "wrapping."

2 _____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ✓ Misaligned Amino Numbering — The numbering under each 5" amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII — The submitted file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length — Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing

6 _____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(ii) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequence.

8 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa and which residue n or Xaa represents.

10 _____ Invalid <211> Response — Per 1.823 of Sequence Rules, the only valid <211> responses are Unknown, Artificial Sequence or scientific name (Genus/species). <220>-<223> section is required when <211> response is Unknown or is Artificial Sequence.

11 _____ Use of <220> — Sequence(s) _____ missing the <220> feature and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <211> Organism response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section (See "Federal Register," 06/01/1998, Vol 63, No 104, pp. 29631-32) (See 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC - Biotechnology Systems Branch - 09/09/2003

BEST AVAILABLE COPY

RAW SEQUENCE LISTING   DATE: 06/02/2005
PATENT APPLICATION: US/10/049,967C   TIME: 08:23:10

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\06022005\J049967C.raw

```
     2 <110> APPLICANT: Imperial College Innovations Limited
W--> 3 <120> TITLE OF INVENTION: Isoforms of Snare Molecules and the Uses Thereof in
W--> 4        Modulation of Cellular Exocytosis
W-->  5 <130> FILE REFERENCE: ICOY/P23294PC
W--> 6 <140> CURRENT APPLICATION NUMBER: US/10/049,967C
     7 <141> CURRENT FILING DATE: 2002-02-18
W--> 8 <160> NUMBER OF SEQ ID: 28
     9 <170> SOFTWARE: PatentIn Ver. 2.0
```

Does Not Comply
Corrected Diskette Needed
(Pg. 1-2)

ERRORED SEQUENCES

```
    26 <210> SEQ ID NO: 3          Found 28
    27 <211> LENGTH: (29)
    28 <212> TYPE: DNA
    29 <213> ORGANISM: Artificial Sequence
W--> 30 <220> FEATURE:
    31 <223> OTHER INFORMATION: Description of Artificial Sequence: pcr primer
W--> 32 <400> SEQUENCE: 3
E--> 33 catcttgtt gcagctgcgt tggcttcat   (29) - 28
    34 <210> SEQ ID NO: 4
    35 <211> LENGTH: (30)    Found 29
    36 <212> TYPE: DNA
    37 <213> ORGANISM: Artificial Sequence
W--> 38 <220> FEATURE:
    39 <223> OTHER INFORMATION: Description of Artificial Sequence: pcr primer
W--> 40 <400> SEQUENCE: 4  (30) delete
E--> 41 catcttgtt gcctttgcgt tggcttcgat   <- 29
    42 <210> SEQ ID NO: 5
    43 <211> LENGTH: (32)   Found 31
    44 <212> TYPE: DNA
    45 <213> ORGANISM: Artificial Sequence
W--> 46 <220> FEATURE:
    47 <223> OTHER INFORMATION: Description of Artificial Sequence: pcr primer
W--> 48 <400> SEQUENCE: 5
E--> 49 agcatcttg ttgcccacca gttggcttca tc   (32) - 31
   162 <210> SEQ ID NO: 20
   163 <211> LENGTH: 10
   164 <212> TYPE: PRT
   165 <213> ORGANISM: Homo Sapiens
   168 <400> SEQUENCE: 20
   169    Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
E--> 170  1    1     5   5              10  10
```

pls group amino acids in sets of 10s

FOR ex°?

atgcctgtgc or aaatgtgctc   20

pls group amino acids in sets of 10s. FOR ex:?

aatgtgccta attccggttc

See item #3 on error summary sheet.

RAW SEQUENCE LISTING   DATE: 06/02/2005
PATENT APPLICATION: US/10/049,967C   TIME: 08:23:10

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\06022005\J049967C.raw**

```
          171 <210> SEQ ID NO: 21
          172 <211> LENGTH: 10
          173 <212> TYPE: PRT
          174 <213> ORGANISM: Artificial Sequence
W-->      175 <220> FEATURE:
          176 <223> OTHER INFORMATION: Description of Artificial Sequence: synthesized
W-->      177 <400> SEQUENCE: 21
          178    Gln Thr Ala Thr Lys Met Leu Gly Ser Gly
E-->      179    1    1       5    5           10  10
          216 <210> SEQ ID NO: 26
          217 <211> LENGTH: 5
          218 <212> TYPE: PRT
          219 <213> ORGANISM: Artificial Sequence
W-->      220 <220> FEATURE:
          221 <223> OTHER INFORMATION: Description of Artificial Sequence: synthesized
          224 <400> SEQUENCE: 26
          225    Gln Arg Ala Thr Lys
E-->      226    1    1       5    5
          227 <210> SEQ ID NO: 27
          228 <211> LENGTH: 5
          229 <212> TYPE: PRT
          230 <213> ORGANISM: Artificial Sequence
W-->      231 <220> FEATURE:
          232 <223> OTHER INFORMATION: Description of Artificial Sequence: synthesized
W-->      233 <400> SEQUENCE: 27
          234    Gln Thr Ala Thr Lys
E-->      235    1    1       5    5
```

See item #3 on error summary sheet.

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/049,967C

DATE: 06/02/2005
TIME: 08:23:11

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\06022005\J049967C.raw

```
L:3 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:283 W: Missing Blank Line separator, <140> field identifier
L:8 M:283 W: Missing Blank Line separator, <160> field identifier
L:10 M:283 W: Missing Blank Line separator, <210> field identifier
L:14 M:283 W: Missing Blank Line separator, <220> field identifier
L:16 M:283 W: Missing Blank Line separator, <400> field identifier
L:22 M:283 W: Missing Blank Line separator, <220> field identifier
L:24 M:283 W: Missing Blank Line separator, <400> field identifier
L:30 M:283 W: Missing Blank Line separator, <220> field identifier
L:32 M:283 W: Missing Blank Line separator, <400> field identifier
L:33 M:254 E: No. of Bases conflict, LENGTH:Input:29 Counted:28 SEQ:3
L:33 M:252 E: No. of Seq. differs, <211> LENGTH:Input:29 Found:28 SEQ:3
L:38 M:283 W: Missing Blank Line separator, <220> field identifier
L:40 M:283 W: Missing Blank Line separator, <400> field identifier
L:41 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:4
L:41 M:252 E: No. of Seq. differs, <211> LENGTH:Input:30 Found:29 SEQ:4
L:46 M:283 W: Missing Blank Line separator, <220> field identifier
L:48 M:283 W: Missing Blank Line separator, <400> field identifier
L:49 M:254 E: No. of Bases conflict, LENGTH:Input:32 Counted:31 SEQ:5
L:49 M:252 E: No. of Seq. differs, <211> LENGTH:Input:32 Found:31 SEQ:5
L:54 M:283 W: Missing Blank Line separator, <220> field identifier
L:56 M:283 W: Missing Blank Line separator, <400> field identifier
L:62 M:283 W: Missing Blank Line separator, <220> field identifier
L:64 M:283 W: Missing Blank Line separator, <400> field identifier
L:70 M:283 W: Missing Blank Line separator, <220> field identifier
L:72 M:283 W: Missing Blank Line separator, <400> field identifier
L:78 M:283 W: Missing Blank Line separator, <220> field identifier
L:80 M:283 W: Missing Blank Line separator, <400> field identifier
L:86 M:283 W: Missing Blank Line separator, <220> field identifier
L:88 M:283 W: Missing Blank Line separator, <400> field identifier
L:94 M:283 W: Missing Blank Line separator, <220> field identifier
L:96 M:283 W: Missing Blank Line separator, <400> field identifier
L:102 M:283 W: Missing Blank Line separator, <220> field identifier
L:104 M:283 W: Missing Blank Line separator, <400> field identifier
L:110 M:283 W: Missing Blank Line separator, <220> field identifier
L:112 M:283 W: Missing Blank Line separator, <400> field identifier
L:118 M:283 W: Missing Blank Line separator, <220> field identifier
L:120 M:283 W: Missing Blank Line separator, <400> field identifier
L:126 M:283 W: Missing Blank Line separator, <220> field identifier
L:128 M:283 W: Missing Blank Line separator, <400> field identifier
L:134 M:283 W: Missing Blank Line separator, <220> field identifier
L:136 M:283 W: Missing Blank Line separator, <400> field identifier
L:142 M:283 W: Missing Blank Line separator, <220> field identifier
L:144 M:283 W: Missing Blank Line separator, <400> field identifier
L:150 M:283 W: Missing Blank Line separator, <220> field identifier
L:152 M:283 W: Missing Blank Line separator, <400> field identifier
L:158 M:283 W: Missing Blank Line separator, <220> field identifier
```

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PATENT APPLICATION: **US/10/049,967C**   TIME: 08:23:11

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\06022005\J049967C.raw**

L:160 M:283 W: Missing Blank Line separator, <400> field identifier
L:170 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:20
L:175 M:283 W: Missing Blank Line separator, <220> field identifier
L:177 M:283 W: Missing Blank Line separator, <400> field identifier
L:179 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21
L:184 M:283 W: Missing Blank Line separator, <220> field identifier
L:186 M:283 W: Missing Blank Line separator, <400> field identifier
L:193 M:283 W: Missing Blank Line separator, <220> field identifier
L:195 M:283 W: Missing Blank Line separator, <400> field identifier
L:202 M:283 W: Missing Blank Line separator, <220> field identifier
L:226 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:26
L:235 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27